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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/964,678A

DATE: 02/06/2002

TIME: 11:39:29

Input Set : A:\seqlist 0609_4370002 ascii
Output Set: N:\CRF3\02062002\I964678A.raw

ENTERED

5 <110> APPLICANT: de la Monte, Suzanne
7 Wands, Jack R.
11 <120> TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs
12 Effective for the Treatment or Prevention of
13 Alzheimer's Disease
17 <130> FILE REFERENCE: 0609.4370002
21 <140> CURRENT APPLICATION NUMBER: 09/964,678A
23 <141> CURRENT FILING DATE: 2001-09-28
27 <150> PRIOR APPLICATION NUMBER: 09/380,203
29 <151> PRIOR FILING DATE: 2000-04-25
33 <150> PRIOR APPLICATION NUMBER: PCT/US98/03685
35 <151> PRIOR FILING DATE: 1998-02-26
39 <150> PRIOR APPLICATION NUMBER: 60/038,908
41 <151> PRIOR FILING DATE: 1997-02-26
45 <160> NUMBER OF SEQ ID NOS: 14
49 <170> SOFTWARE: PatentIn version 3.1
53 <210> SEQ ID NO: 1
55 <211> LENGTH: 1442
57 <212> TYPE: DNA
59 <213> ORGANISM: Unknown
63 <220> FEATURE:
65 <223> OTHER INFORMATION: AD7c-NTP cDNA
67 <220> FEATURE:
69 <221> NAME/KEY: CDS
71 <222> LOCATION: (15)..(1139)
73 <223> OTHER INFORMATION:
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82 aat ggc gca atc tca gct cac cgc aac ctc cgc ctc ccg ggt tca agc 98
83 Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser 25
84 15 20 25
86 gat tct cct gcc tca gcc tcc cca gta gct ggg att aca ggc atg tgc 146
87 Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys 40
88 30 35 40
90 acc cac gct cgg cta att ttg tat ttt ttt tta gta gag atg gag ttt 194
91 Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe 60
92 45 50 55
94 ctc cat gtt ggt cag gct ggt ctc gaa ctc ccg acc tca gat gat ccc 242
95 Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro 75
96 65 70
98 tcc gtc tcg gcc tcc caa agt gct aga tac agg act ggc cac cat gcc 290

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PATENT APPLICATION: US/09/964,678A

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Input Set : A:\seqlist_0609_4370002 ascii
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102 cgg ctc tgc ctg gct aat ttt tgt ggt aga aac agg gtt tca ctg atg 338
103 Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met
104      95      100      105
106 tgc cca agc tgg tct cct gag ctc aag cag tcc acc tgc ctc agc ctc 386
107 Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu
108      110      115      120
110 cca aag tgc tgg gat tac agg cgt gca gcc gtg cct ggc ctt ttt att 434
111 Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile
112 125      130      135      140
114 tta ttt ttt tta aga cac agg tgt ccc act ctt acc cag gat gaa gtg 482
115 Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val
116      145      150      155
118 cag tgg tgt gat cac agc tca ctg cag cct tca act cct gag atc aag 530
119 Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys
120      160      165      170
122 cat cct cct gcc tca gcc tcc caa gta gct ggg acc aaa gac atg cac 578
123 His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His
124      175      180      185
126 cac tac acc tgg cta att ttt att ttt att ttt aat ttt ttg aga cag 626
127 His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln
128      190      195      200
130 agt ctc aac tct gtc acc cag gct gga gtg cag tgg cgc aat ctt ggc 674
131 Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly
132 205      210      215      220
134 tca ctg caa cct ctg cct ccc ggg ttc aag tta ttc tcc tgc ccc agc 722
135 Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser
136      225      230      235
138 ctc ctg agt agc tgg gac tac agg cgc cca cca cgc cta gct aat ttt 770
139 Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe
140      240      245      250
142 ttt gta ttt tta gta gag atg ggg ttc acc atg ttc gcc agg ttg atc 818
143 Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile
144      255      260      265
146 ttg atc tct gga cct tgt gat ctg cct gcc tcg gcc tcc caa agt gct 866
147 Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala
148      270      275      280
150 ggg att aca ggc gtg agc cac cac gcc cgg ctt att ttt aat ttt tgt 914
151 Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys
152 285      290      295      300
154 ttg ttt gaa atg gaa tct cac tct gtt acc cag gct gga gtg caa tgg 962
155 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp
156      305      310      315
158 cca aat ctc ggc tca ctg caa cct ctg cct ccc ggg ctc aag cga ttc 1010
159 Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe
160      320      325      330
162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cac ctg cca cca 1058
163 Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro

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164          335          340          345          1106
166 cac ccc gct aat ttt tgt att ttc att aga ggc ggg gtt tca cca tat
167 His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr
168          350          355          360          1159
170 ttg tca ggc tgg tct caa act cct gac ctc agg tgaccacct gcctcagcct
171 Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg
172 365          370          375          1219
174 tccaaagtgc tgggattaca ggcgtgagcc acctcaccca gccggctaatt ttagataaaa
176 aaatatgtag caatgggggg tcttgctatg ttgccaggc tggctctcaaa cttctggcctt
178 catgcaatcc ttccaaatga gccacaacac ccagccagtc acatttttta aacagttaca
180 tctttatttt agtatactag aaagtaatac aataaacatg tcaaacctgc aaattcagta
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187 <211> LENGTH: 375
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191 <213> ORGANISM: Unknown
195 <220> FEATURE:
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206          20          25          30
209 Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
210          35          40          45
213 Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
214          50          55          60
217 Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
218 65          70          75          80
221 Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu
222          85          90          95
225 Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
226          100          105          110
229 Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
230          115          120          125
233 Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
234          130          135          140
237 Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp
238 145          150          155          160
241 His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
242          165          170          175
245 Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
246          180          185          190
249 Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
250          195          200          205
253 Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
254          210          215          220
257 Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
258 225          230          235          240

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261 Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
 262 245 250 255
 265 Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
 266 260 265 270
 269 Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
 270 275 280 285
 273 Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
 274 290 295 300
 277 Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
 278 305 310 315 320
 281 Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
 282 325 330 335
 285 Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
 286 340 345 350
 289 Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp
 290 355 360 365
 293 Ser Gln Thr Pro Asp Leu Arg
 294 370 375

297 <210> SEQ ID NO: 3

299 <211> LENGTH: 1381

301 <212> TYPE: DNA

303 <213> ORGANISM: Unknown

307 <220> FEATURE:

309 <223> OTHER INFORMATION: Incorrect sequence of AD7c-NTP DNA

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 314 ctcagctcac cgcaacctcc gcctcccggg ttcaagcgat tctcctgcct cagcctcccc 120
 316 agtagctggg attacaggca tgtgcaccac gctcggctaa ttttgatttt ttttttagta 180
 318 gagatggagt ttaactccat gttggtcagg ctggctcga actcccgacc tcagatgatc 240
 320 tcccgtctcg gcctgcccaa agtgcctgaga ttacaggcat gagccaccat gccgggcctc 300
 322 tgccctggcta atttttgtgg tagaaacagg gtttactga tgttgcccaa gctggctctc 360
 324 tgagctcaag cagtcacact gcctcagcct cccaaagtgc tgggattaca ggcgtcagcc 420
 326 gtgcctggcc tttttatttt atttttttta agacacagg gtaccactct taccaggat 480
 328 gaagtgcagt ggtgtgatca cagctcactg cagccttcaa ctctgagat caagcaatcc 540
 330 tcctgcctca gcctcccaa tagctgggac caaagacatg caccactaca cctggtaatt 600
 332 tttattttta tttttaattt tttgagacag agtctcactc tgtcaccag gctggagtgc 660
 334 agtggcgcaa tcttggtcga ctgcaacctc tgccctcccg gttcaagtta ttctcctgcc 720
 336 ccagcctcct gagtagctgg gactacaggc gccaccacg cctagctaat ttttttgcct 780
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 340 gatctgcctg cctcggccta cccaaagtgc tgggattaca ggtcgtgact ccacgcgggc 900
 342 ctatttttaa tttttgtttg tttgaaatgg aatctcactc tggtaccag gtcggagtgc 960
 344 aatggcaaat ctcggtact cgcaacctct gcctcccggg tcaagcgatt ctctgtctc 1020
 346 agcctcccaa gcagctggga ttacgggacc tgcaaccac cccgctaatt tttgtatttt 1080
 348 cattagaggc gggtttacca tatttgcag gctgggtctc aaactcctga cctcaggtga 1140
 350 cccacctgcc tcagccttcc aaagtgcagg gattacaggc gtgagccacc tcaccagcc 1200
 352 ggctaatttg gaataaaaaa tatgtagcaa tgggggtctg ctatgttgcc caggctggtc 1260
 354 tcaaaacttct ggcttcagtc aatccttcca aatgagccac aacaccagc cagtcacatt 1320
 356 ttttaaacag ttacatcttt attttagtat actagaaagt aatacaataa acatgtcaaa 1381

358 c

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DATE: 02/06/2002
TIME: 11:39:29Input Set : A:\seqlist 0609_4370002 ascii
Output Set: N:\CRF3\02062002\I964678A.raw

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361 <210> SEQ ID NO: 4
363 <211> LENGTH: 1418
365 <212> TYPE: DNA
367 <213> ORGANISM: Unknown
371 <220> FEATURE:
373 <223> OTHER INFORMATION: Incorrect sequence of AD7c-NTP cDNA
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378 ctcagctcac cgcaacctcc gcctcccggg ttcaagcgat tctcctgcct cagcctcccc 120
380 agtaggctgg gattacaggc atgtgcacca cgctcggcta attttgatt ttttttagt 180
382 agagatggag tttctccatg ttggtcaggc tggctcgaac ctccgacctc agatgatcct 240
384 cccgtctcgg cctcccacaa tgctagatac aggactgagc accatgcccg gcctctgcct 300
386 ggctaatttt tgtggtagaa acagggtttc actgatgtgc ccaagctggg ctctgagct 360
388 caagcagtc acctgcctca gcctcccaaa gtgctgggat tacaggcgtg cagccgtgcc 420
390 tggccttttt attttatttt ttttaagaca cagggtgtcc actcttacc aggatgaagt 480
392 gcagtgggtg gatcacagct cactgcagcc ttcaactctg agatcaagca tcctcctgcc 540
394 tcagcctccc aaagtagctg ggaccaaaga catgcaccac tacacctggc taatttttat 600
396 tttttatttt aattttttga gacagagtct caactctgtc acccaggctg gagtgcagtg 660
398 gcgcaatctt ggctcactgc aacctctgcc tcccgggttc aagttattct cctgccccag 720
400 cctcctgagt agctgggact acaggcgccc accacgccta gctaattttt ttgtattttt 780
402 agtagagatg gggtttcacc atgttcgcca ggttgatgct agatctcttg acctgtgat 840
404 ctgcctgcct cggcctccca aagtgtctgg attacaggac gtgacgccc cgcgccggcc 900
406 tatttttaat ttttgttgtg ttgaaatgga atctcactct gttaccagg ctggagtgca 960
408 atggccaaat ctcggtctac tgcaacctct gcctcccggg ctcaagcgat tctcctgtct 1020
410 cagcctccca agcagctggg attacgggca cctgcaccac accccgctaa tttttgtatt 1080
412 ttcattagag gcgggggttt accatatttg tcaggtgggt ctcaaactcc tgacctcagg 1140
414 tgaccacact gcctcagcct tccaaagtgc tgggattaca ggcgtgacgc ctcaccaggc 1200
416 cggctaattt agataaaaaa atatgtagca atgggggggtc ttgctatgtt gccaggctg 1260
418 gtctcaaaact tctggcttca tgcaatcctt ccaaattgagc cacaacacc agccagtcac 1320
420 atttttaaac agttacatct ttattttagt atactagaaa gtgatacgat aacatggcgg 1380
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427 <211> LENGTH: 22
429 <212> TYPE: DNA
431 <213> ORGANISM: Artificial Sequence
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437 <223> OTHER INFORMATION: AD7c-NTP oligonucleotide
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443 <210> SEQ ID NO: 6
445 <211> LENGTH: 24
447 <212> TYPE: DNA
449 <213> ORGANISM: Artificial Sequence
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455 <223> OTHER INFORMATION: AD7c-NTP oligonucleotide
457 <400> SEQUENCE: 6
458 aagcaggcag atcacaaggt ccag
461 <210> SEQ ID NO: 7
463 <211> LENGTH: 20

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22

24

→ Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14